Fatty acid oxidation is impaired in an orthologous mouse model of Autosomal Dominant Polycystic Kidney Disease

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Supplementary Figures.

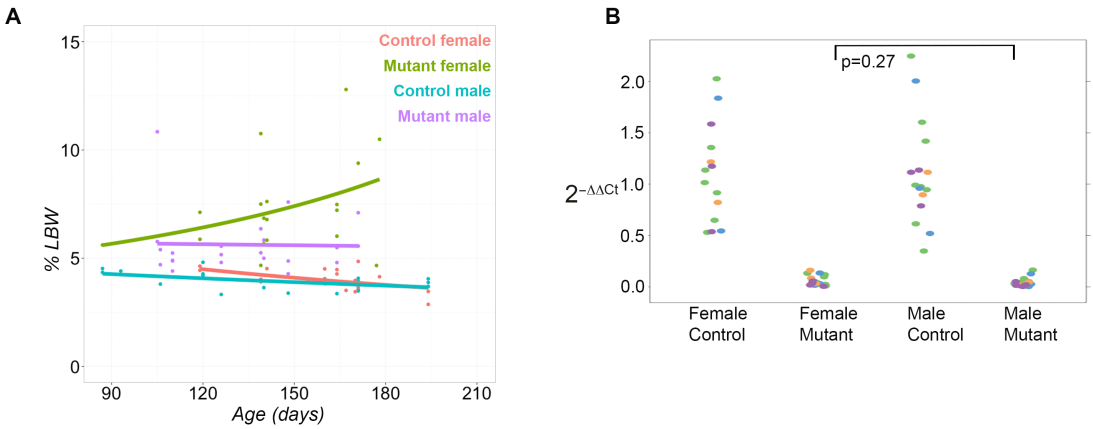

Figure S1. Liver phenotype and *Pkd1* inactivation rates. A) Liver to body weight ratios (LBW) plotted over time starting 60 days after *Pkd1* inactivation and showing more severe liver disease in females. B) Reverse transcription PCR showing similar rate of *Pkd1* inactivation in male and female mutant kidneys (normalized within sex; p=0.27). Each dot corresponds to the sample average (3 or 4 replicates) for each independent experiment and is colored by experimental batch (i.e. independent time the experiment was repeated). Number of independent samples: control female-7; mutant female-11; control male-8; mutant male-12.

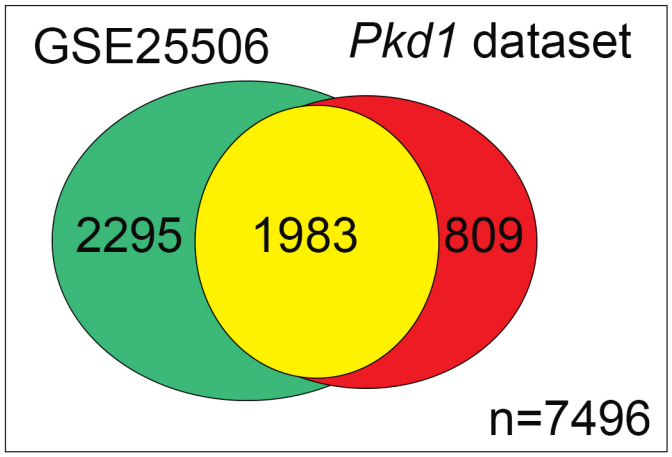

Figure S2. Independent dataset confirms sexually dimorphic gene expression in mouse kidney. Out of 7496 genes expressed in both GSE25506 and the current "*Pkd1* dataset", comparisons using only control animals showed differential expression of 4278 genes (57% of all expressed genes; green and yellow) in GSE25506, 2793 in the "*Pkd1* dataset" with an overlap of 1983 genes (26%) differentially expressed in both datasets (in yellow).

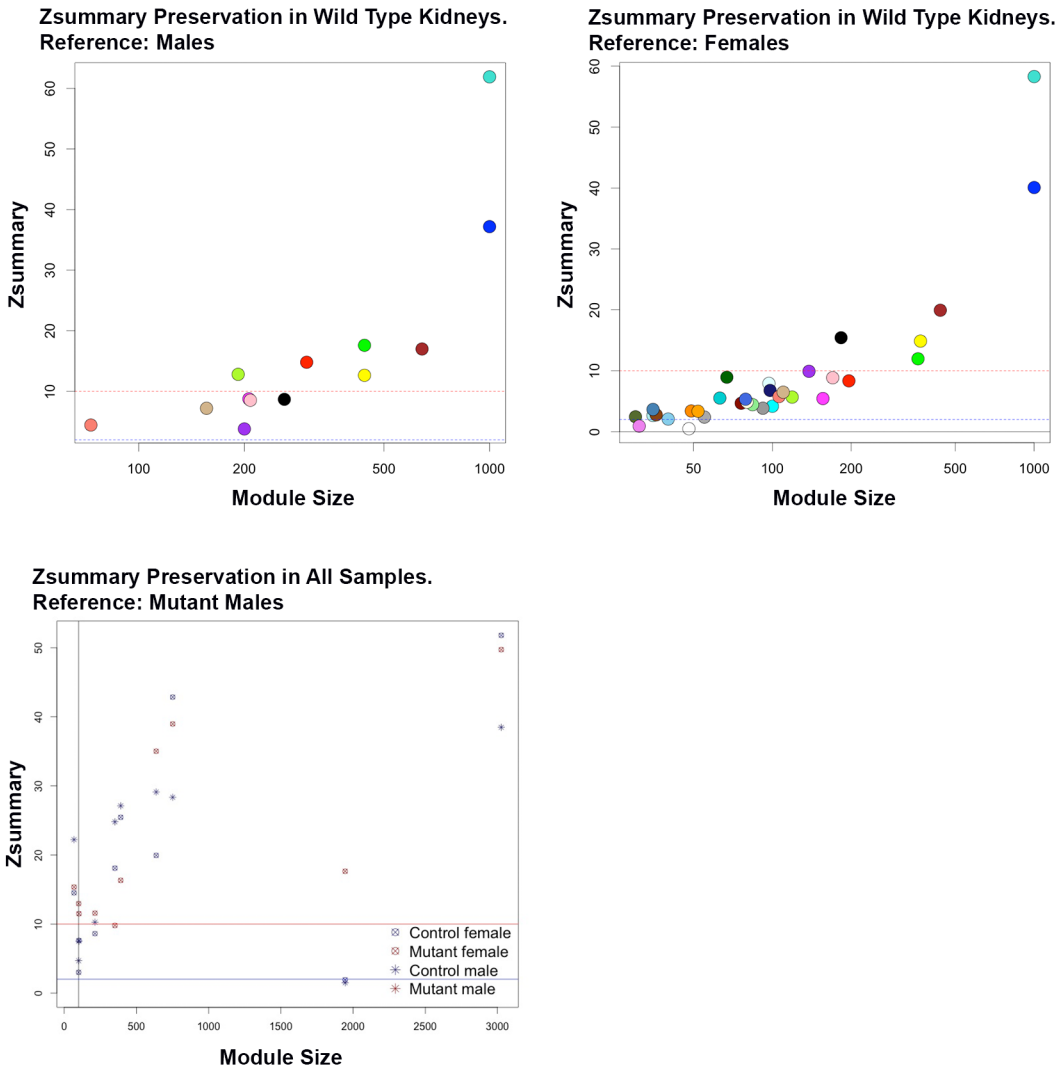

Figure S3. Networks are preserved. Each dot represents a module inferred in the corresponding reference dataset. Zsummary scores the presence of similar modules inferred using other samples (for instance, on the left most panel, modules identified in wild type male kidneys are scored for preservation in wild type female kidneys; in that case, a module colored turquoise has >1000 genes and is highly preserved between males and females, as reflected by a Zsummary score of ~60). A value above 2 (blue

line) or above 10 (red line) is considered indication of preserved or highly preserved module, respectively. While small modules are less preserved, the majority of modules in all networks are preserved between sexes (two top panels) and between mutant and control samples (lower panel). Dots in the two top panels are colored by module name; in the lower panel, by group.

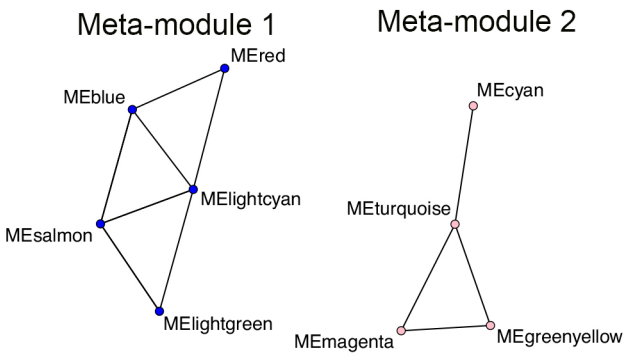

Figure S4. Sex meta-modules are formed by correlated modules. Each dot (node) represents a module (or cluster) of genes with highly correlated expression patterns. The edges linking these nodes represent further correlation between the modules. This analysis shows that the genes differentially expressed between control male and female kidneys can be grouped into two large clusters of highly correlated genes, which we labeled “Meta-module 1” and “Meta-module 2”. These meta-modules are highly enriched in metabolic gene ontology categories (see text and Supplementary Table 1.).

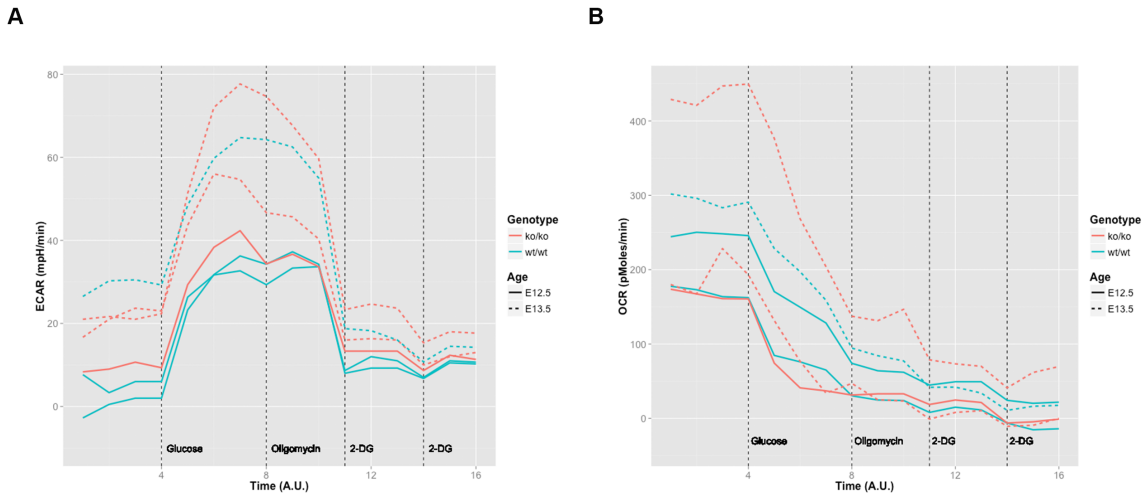

Figure S5. Glycolysis rate is similar in mouse embryonic fibroblasts. Plots showing A) extracellular acidification rate (ECAR) and B) oxygen consumption rate (OCR) in mouse embryonic fibroblasts (MEF) of E12.5 and E13.5 mutant and control embryos. The vertical dashed lines represent the sequential addition of glucose, oligomycin, and 2-deoxy-glucose (2-DG).